Sequence:

Run on:

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                        OM nucleic - nucleic search, using sw model
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Perfect score:
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em\_htg9:\*
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em\_htg10:\*
em\_hum3:\* em\_hum4: \*\*
em\_hum6: \*\*
em\_hum gb\_vil:\*
gb\_vi2:\*
gb\_patl:\*
gb\_pat2:\*
em\_htg0:\*
gb\_htg24:\* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	AE002409 Neisseria		AX011572 Sequence		U32853 Pseudomonas	U49151 Pseudomonas	AE004511 Pseudomon	U30799 Azotobacter	AE004037 Xylella f	AX011580 Sequence	AF293977 Aeromonas	AE004859 Pseudomon	U31512 Rhizobium m	U07352 Brucella ab	L09274 Brucella ab	AE004142 Vibrio ch	U32495 Escherichia	U15661 Escherichia	AE000402 Escherich
SUMMARIES	AE002409 AX011576	NMA3Z2491	AX011572	AX011578	PAU32853	PAU49151	AE004511	AVU30799	AE004037	AX011580	AF293977	AE004859	RMU31512	BAU07352	BRUHTRAH	AE004142	ECU32495	ECU15661	AE000402
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s Query Match	94.8	94.3	90.2	76.1	26.2	26.2	26.2	19.7	18.7	18.7	17.6	15.6	15.2	15.2	14.1	14.1	14.1	14.1	14.1
Score	1322.2	1315.8	1258.2	1061	365.6	365.6	365.6	274.8	260.4	260.2	246	217.4	212.4	211.8	197	196.6	196	196	196
ult No.	7 7	σ 4	. 2	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21
Result No.	υ	ပ														υ			

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Continuation (2 of U29172 Pseudomonas AF163841 Myxococcu AB040030 Shigella AE000125 Escherich D2662 Escherichia U70214 Escherichia AR095624 Sequence X12458 E.coli http X54548 S.typhimuri AR0347634 Sequence AR0404795 Sequence AR0404795 Sequence AR0404795 Sequence AR0404795 Sequence	A18802 btrA gene. Y11304 R.capsulatu D78376 Yersinia en U07351 Brucella ab AR000272 Sequence 151141 Sequence 1518681 Sequence L20127 Rochalimaea	AE001355 Chiamydia Y13616 Bradyrhizob	BCT 25-MAY-2000 strain MC58 section 51 of 206 of	vision; Neisseriaceae;	rgy.v., Jettries, A.C., ', Hood, D.W., Peden, J.F., ', DeBoy, R., Peterson, J.D., ', White, O., Fleatschmann, R.D., Parksey, D.S., Blair, E., Utterback, T.R., Khourt, H., lato, V., Masignani, V., 'O., Fraser, C.M., Moxon, E.R., a meningitidis serogroup B	rg,J., Jeffries,A.C., ., Hood,D.W., Peden,J.E., ., DeBoy,R., Petersson,J.D., ., White,O., Eleischmann,R.D., Parksey,D.S., Blair,E., Utterback,T.R., Khouri,H., Outerback,T.R., Khouri,H.,	e for Genomic Research, 9712 50, USA itidis MC58"
22 196 14.1 110000 2 ECOUM67_1 23 186.6 13.4 1191 2 PAU29172 25 181.2 13.0 1476 1 AF165841 26 178 12.8 10199 1 AE000125 27 178 12.8 12377 2 ECU70214 29 176.4 12.6 1855 2 ECUTRA 30 176.4 12.6 1855 2 ECUTRA 31 176.6 12.6 1980 29 STSPHSPG 33 175.6 12.6 1980 29 STSPHSPG 34 175.6 12.6 1980 81 AR037634 37 175.6 12.6 1980 81 AR037634	175.2 12.6 1980 81 164.6 11.8 1808 2 157.2 11.3 1613 2 154.2 11.1 1791 81 154.2 11.1 1791 81 154.2 11.1 1791 82 154.2 11.1 1791 82 154.2 11.1 1791 82 164.2 11.1 1791 82	148.2 10.6 11881 147.6 10.6 2778	AEGO2409/c LOCUS AEGO2409 10531 bp DNA DEFINITION Nelsseria meningitidis serogroup B s ACCESSION AEGO2409 AEGO2098 VERSION AEGO2409.1 GI:7225757	KEYWORDS SOURCE SOURCE Neisseria meningitidis MC58. ORGANISM Neisseria meningitidis MC58 Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria. REFERENCE I (bases I to 10531) AUTHORS Tettolin.H. Sannders.N. I. Heidelberg I Jeffries A C	AUTHORS JELUELLIN, SAUTHORES, N. J., HELGELDERGY, J., JELLES, N. J., MESON, K.E., Eisen, J.A., Ketchum, K.A., Hood, D.W., Peden, J.F., Dodson, R.J., Nelson, W.C., Gwinn, M.L., DeBoy, R., Peterson, J.D., Hickey, E.K., Haft, D.H., Salzbergy, S.L., White, O., Fleischmann, R.D. Dougherty, B.A., Mason, T., Ciecko, A., Parksey, D.S., Blair, E., Cittone, H., Clark, E.B., Cotton, M.D., Utterback, T.R., Khouri, H., Pizza, M., Grandi, G., Sun, L., Smith, H.O., Fraser, C.M., Moxon, E.R., Rappuoli, R. and Venter, J.C.  TITLE Complete genome sequence of Neisseria meningitidis serogroup B strain MC58  Strain MC58  JOURNAL Science 287 (5459), 1809-1815 (2000)		Rappuoli, R. and Venter, J.C.  TITLE Direct Submission JOURNAL Submitted (17-MAR-2000) The Institute for Genom Medical Center Dr., Rockville, MD 20850, USA Location/Qualifiers 1. 10531 /organism="Neisseria meningitidis MC58 /strain="MC58"

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gene

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KTIIRTLYSNPASHGANTIALVLKNDDLKAQWIAELDEMRGRIKAMRQKFVGLLKAKG
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                                     Score 1322.2; DB 1;
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Oy 181 gt	Oy 241 aau 	Oy 301 gas   1     Db 301 GA	Qy 361 gg	Oy 421 ac       Db 421 AC	Qy 481 ac	Qy 541 acc	Oy 601 gt.	661	Db 661 GC( Oy 721 atc	Db 721 AT	Oy 781 aa 	Oy 841 gae	901	Db 901 CTC QY 961 gcc	Db 961 GC	1021	Oy 1081 cco	Oy 1141 990   Db 1141 GG	Oy 1201 tcc	
Oy 961 gccagcggcgcattgattgccaaaatccttcccggcagcccgcagaacgtgccggcctg 1020 	Oy 1021 caggoggogacatcgtcctcagcctcgacggoggagaaatacgttcttccggogacctt 1080 	Oy 1081 cccgtcatggtcggcgcttacgccgggaaaagaagtcagcctcggcgtatggcgcaaa 1140 	Oy 1141 ggcgaagaaatcacaatcaaagccaagctgggcaacgccgcgggcataccggcgcatca 1200 	Oy 1201 tccaaaacagatgaagcccctacaccgaacagcaatccggtacgtctcggtcgaatcc 1260 	Oy 1261 gcaggcattaccttcagacacataccgacagcagcagcggcaaacacctcgtcgtcgtacgg 1320 	Qy 1321 gtttccgacgcggcagaacgcgcaggcttaaggcacggcgacgaatcctagccgtcagg 1380 	Oy 1381 gcaagtcccgtcaa 1395 	RESULT 2	AX011576 LOCUS AX011576 1500 bp DNA BCT 18-SEP-2000 DEFINITION Sequence 5 from Patent W0995872. ACCESSION AX011576	VERSION AX011576.1 GI:9998107 KEYWORDS .	SOURCE Neisseria meningitidis. ORGANISM Neisseria meningitidis Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;	REFERENCE 1 (bases 1 to 1500) AUTHORS Ruelle,J.L. TITLE Rash013 dna and proteins from peisseria meningitidis	Patent: WO 9955872-A 04-NOV-1999; RUELLE JEAN LOUIS (BEB); SHITHKLINE BEECHAM BIOLOG (	source /organism-"Neisseria meningitidis" /db_xref-"taxon:487"	BASE COUNT 585 & 4/1 C 582 g 262 C ORIGIN	Query Match  Query Match  Best Local Similarity 97.1%; Pred. No. 3.4e-234;  Matches 1355; Conservative 0; Mismatches 39; Indels 1; Gaps 1;	<pre>Qy 1 gtgttcaaaaaataccaatacttcgctttggcggcactgtgtgccgccttgctggcaggc 60</pre>	Oy 61 tgcgaaaaggcaggcattttcggtgcggacaaaaagaagcatccttcgtagaacgc 120 	Oy 121 atcgaacaccaaagacgacggcagtctcagtatgctgctgcccgactttgcccaactg 180 	

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us-09-388-090-3.rge

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                                                                                                                                                                                                                                                                                              NMA322491 311321 bp DNA BCT 30-MAR-2000
Neisseria meningitidis serogroup A strain 22491 complete genome;
segment 3/7.
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Centre are
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Parkhill, J., Achtman, M., James, K.D., Bentley, S.D., Churcher, C. Riee, S.R., Morelli, G., Basham, D., Brown, D., Chillingworth, T., Davis, R.M., Davis, P., Devlin, K., Feltwell, T., Hamlin, N., Holroyd, S., Jagels, K., Leather, S., Moule, S., Mingall, K., Coail, M.A., Rajandream, M.A., Rutherford, K.M., Simmonds, M., Skelton, J., Whitehead, S., Spratt, B.G. and Barrell, B.G. Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (30-MAR-2000) Submitted on behalf of the Neisseria
sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk
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/gene="NMA0699"
/note="NMA0699, pseudogene, probable ABC transporter
                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis.
Neisseria meningitidis
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;
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(URL, http://www.sanger.ac.uk/Projects/N_meningitidis/).
Location/Qualifiers
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/strain="22491"
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742. .1077
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AL162754.2 GI:7379424
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Complement(1101. 2327)

/gene="NMA0700" 2327)

/gene="NMA0700" 2327)

/gene="NMA0700" 2327)

/gene="NMA0700" possible ribonuclease BN, len: 408 aa;

/gene="NMA0700" possible membrane-spanning regions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MYFLORLOGLADNKICAFAWFVVRRFDEERVPQAAASMTFTTLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FCLETARSLFTWYMÖNFDGYRSIYGAPAAVPFFLLMLNILWTLWTLULGGAVITSSLSYWO
GEARRRGFDSRGRFDDVLKILLLLDAAQKEGKALPVQEFRRHINMGYDELGELLEKLA
RHGYIYSGRQGWVLKTGADSIELNELFKLFVYRPLPVERDHVNQAVDAVMMPCLQTLN
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                                                                                                                                                                                                                                   /transl_table=11
/product="putative ABC transporter protein (pseudogene)"
868. .912
/gene="NMA0699"
                    to C-termini of many ABC
protein, len: 336 bp; similar to C-termini of many ABi transporters e.g. TR:046973 (EMBL:047048), mtfB, Escherichia coli microcin transport protein (707 aa), fasta scores; E(): 2.6e-19, 53.2% identity in 111 aa overlap. Contains PS00211 ABC transporters family signature. NMA0686 may be the remainder of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NMA0701 (pseudogene)"
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/note="Core DNA uptake sequence: gccgtctgaa"
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1376. 11885
/note="Core DNA uptake sequence: gccgtctgaa"
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/note="Core DNA uptake sequence: gccgtctgaa"
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/product="hypothetical
                                                                                                                                                                                                                                                                                                                                                                    /note="PS00211 ABC
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2486. 2743
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2861. 2864 2871. 3530 /gene-"NMA0702" 2871. 3530 /gene-"NMA0702" /note-"NMA0702" /note-"Nypotherical protein NMA0702" /protein_id-"CAB83989.1" /product-"Nypotherical protein NMA0702" /protein_id-"CAB83989.1"	79.2. 79.2. 70.2.	782. 3791  /gene."NMA0703"  /note."Core DNA uptake sequence: gccgtctgaa" /note."Pfam match to entry PF01242 PTPS, 6-pyruvoy1 tetrahydropterin synthase, score 10.80, E-value 1.7e-06" /gene."NMA0704" /083. 4505 /gene."NMA0704" /083. 4505 /gene."NMA0704, len: 140 aa: similar to many hypothetical proteins e.g. SW:YB90_HAEIN (EMBL:U32798), HI1190, faste."NMA0704, len: 140 aa: similar to eukaryottic proteins e.g. SW:YB90_HAEIN (EMBL:U32798), HI1190, fasta scores: E(): 5.1e-32, S8.0% identity in 138 aa overlap. Shows very weak similarity to eukaryottic fermalydrobiopterin synthases e.g. SW:PTPS_RAT (EMBL:M77850), pts, Rattus norvegicus 6-pyruvoy1 tetrahydropterin synthase precursor (EC 4.6.1.10) (144 aa), fasta scores: E(): 0.0062, 27.3% identity in 154 aa overlap. Contains Pfam match to entry PF01242 PTPS, //ransl_table-11 //ransl_table-11 //product=*hypothetical protein NMA0704"	94.3%; Score 1315.8; DB 2; Length 311321; Larity 96.9%; Pred. No. 8.5e-234; Conservative 0; Mismatches 42; Indels 1; Gaps 1;
RBS gene CDS	misc_feature RBS gene CDS	misc_feature misc_feature gene CDS	Query Match Best Local Similarity Matches 1352; Conser

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	RESULT 5 AX011572 LOCUS DEFINITION Sequence 1 from Patent W09955872. ACCESSION AX011572 GI:9998105 VERSION AX011572.1 GI:9998105	SOURCE Neisseria meningitidis. SOURCE ORGANISM Neisseria meningitidis Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria. REFERENCE 1 (bases 1 to 1500)	AUTHORS Ruelle, J.L. TITLE Basb013 dna and proteins from neisseria m JOURNAL Patent: WO 995872-A 04-NOV-1999; RUELLE JEAN LOUIS (BE); SMITHKLINE BEECHA EATURES Source 1. 1500	An an analysis of the section menting that the section of the sec	Query Match 90.2%; Score 1258.2; DB 2; Length 1500; Best Local Similarity 94.3%; Pred. No. 1.1e-222; Matches 1316; Conservative 0; Mismatches 78; Indels 1; Gaps 1;	Qy l gtgttcaaaaataccaatacttcgctttggcgcactgtgtgccgccttgctggcaggc 60	Oy 61 tgcgaaaaggcaggcagcttttcggtgcgacaaaaagaagcatccttcgtagaacgc 120 	Oy 121 atcgaacaccaaagacgacggcagtgtcagtatgctgctgcccgactttgcccaactg 180 	Qy 181 gttcaaagcgaaggccggcagtcgtcaatattcaggcagccccgcgcgcacccaa 240	Oy 241 aacggcagcggcaatgccgaaaccgattccgaccgcttgccgacagcgacccgttctac 300	Oy 301 gaattitcaaacgcctcgtcccgaacatgcccgaaatcccccaagaagaagaagagag 360 	Qy 361 ggcggattgaacttcggttcgggcttcatcatcagcaaaacggctacatcctgaccaat 420 	Qy 421 acccacgtcgttgccggtatgggcagtatcaaagtcctgctcaacgacaagcgcgaatat 480	Qy 481 accgccaaactcatcggttcggatgtccaatccgatgtcgccttctgaaaatcgacgca 540	Oy 541 acggaagagctacccgtcgtcaaatcggcaatcccaaaatttgaaaccgggcgaatgg 600 	Qy 601 gtcgctgccatcggcgcccttcggctttgacaacagcgtgaccgccggcatcgtgtcc 660

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Boucher, J.C., Martinez-Salazar, J., Schurr, M.J., Mudd, M.H., Yu, H. and Deretic, V.
Two distinct loci affecting conversion to mucoidy in Pseudomonas aeruginosa in cystic fibrosis encode homologs of the serine
                                                          06-MAR-1996
complete cds.
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                                                                                                  Pseudomonas aeruginosa.
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Bacteria; Proteobacteria; gamma
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Submitted (31-UUL-1995) John C.
of Texas Health Science Center,
TX 78240, USA
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PAU49151 4587 bp DNA BCT 13-MAR-1996
Pseudomonas aeruginosa alternate sigma factor (algU), mucA, mucB, mucC and mucD genes, complete cds.
U49151 U24569 U6380 L04794 L02119
U49151.1 GI:1220191

LOCUS

ACCESSION VERSION

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Schurr, M.J., Yu, H., Boucher, J.C., Hibler, N.S. and Deretic, V. Multiple promoters and induction by heat shock of the gene encoding the alternative sigma factor Algu (sigma E) which controls mucoidy in cystic fibrosis isolates of Pseudomonas aeruginosa J. Bacteriol. 177 (19), 5670-5679 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (09-FEB-1996) John C. Boucher, Microbiology, U.T. HSC San Antonio, 7703 Floyd Curl Dr., San Antonio, Tx 78284, USA On Mar 11, 1996 this sequence version replaced gi:1173501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          end is
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Martin, D.W., Schurr, M.J., Yu, H. and Deretic, V.
Analysis of promoters controlled by the putative sigma factor Algu
regulating conversion to mucody in Pseudomonas aeruqinosa:
relationship to sigma E and stress response
J. Bacteriol. 176 (21), 6688-6696 (1994)
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Boucher,J.C., Martin,D.W., Schurr,M.J., Deretic,V., Yu,H., Mudd,M
and Martinez-Salizar,J.
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Mudd,M.H. and Deretic,V.
Differentiation of Pseudomonas aeruginosa into the
alginate-producing form: inactivation of mucB causes conversion
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7. (Dassa 1 to 4587)
Boucher, J.C., Martinez-Salazar, J., Schurr, M.J., Mudd, M.H., Yu, H.
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                                                            Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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Proc. Natl. Acad. Sci. U.S.A. 90 (18), 8377-8381 (1993)
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                                                                                                            1 (bases 409 to 1055)
Martin, D. W. Holloway, B. W. and Deretic, V.
Characterization of a locus determining the
Pseudomonas aeruginosa: Algu shows sequence
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/db_xref-"taxon:287'
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Pseudomonas aeruginosa
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/traislation="MITLKRCMAAMVALLALSLAMTARAELDDFTPLVEQASPAVVNI
STROKLPDRAMARGQLSIPDLEGLPPWFRDFLERSIPOVPRNPRGQOREAGSLGSGFI
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GDSWIKLKVGEWVLAIDSPFCFILVRNSTOFRSHPRSVAVKI ERAKNLPTLKL
GDSWICLKVGEWVLAIDSPFCFINSTORIVAGIVSRSHPRSVYPFIOTDVAINFGNSG
GPLLNLGGEVVGINSQIFTRSGGFMGLSFAIPIDVALNVADOLKKAGKVSRGWLGVVI
ORVNKDLAESFCLDKPSGSALVAQLVEDGPAARGCLQVGDVILSLNGQSINESADLPHL
VGNMKFQDRXINLDVIRNGQRKSLSMAVGSLPDDEEIASMGAPGAERSSNRLGVYVAD
LITARQRKSLDIGGGVVIKEVQRGPAAVIGLRPGDVITHLDNKAVTSTKVFADVARALP
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VGAGRARVRALSDLSLRVGDAVVLGIHEDLLLRASVLFYLFPLLGFFVAALLATRAGL
VEPLIIVSGLAGLLAAWLLVRRHARRHADDPASQPVVLRALISGPSDSA"
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/transl_table=11
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/db_xref="GI:1173503"
/db_xref="GI:11735
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QLWPRKEPDPSQLASWYDLRLVGESYRYGRRPAVLAVATVBROGHRYGEFLLDROTGLP
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LRPGFFLTRESPMRSPYTPDPVACLTYGDGLARFSVFIEPLHGAMVGDARSQLGFTVV
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promoters; Algu-dependent promoters strongly resemble
signat promoters of E. coll in both the -10 and -35
sequences"
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/function="conversion to mucoidy; required for algD
transcription"
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     /note="transcription start site for promoter P4; 3'
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                                                                                                                                                                                                                  /note="AlgU-dependent transcription start site for promoter P3; 3' end is unknown"
                                                                                                                                                                                                                                                                                                                                                                   promoter P2;
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2627. .3082
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promoter P3; 3' end is unknown"
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                                                     204. .238
/note="P3 promoter"
204. .209
/note="P3 promoter"
226. .230
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/note="P1 promoter"
389. .421
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/note="Pl promoter"
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/gene="mucB"
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/transl_table=11
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/transl_table=11
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474. .1055
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1680.
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1087.
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GNSGOGTAMAWRAGCKRONLEPNOFHPTCLYHOPASFELLTEALRGGEALBLLPNGER
FWPRPDRAGELARRDIVARALDHEKKRLGIDOYYLDISHKPAEFIKAHFPTYVERCLD
FGIDITQOPIPVVPAAHYTGGGVLVDOHGHTDVPGLYAIGETTFTGLHGANRMASNSL
LECFYARRAADAMACRLPGTPVPESLESENDASOVTDSDEDVIIAINWDELRRFWWDY
VGIVYRTKRLQYRADHRYRLLLSEIDDEFYSNYKVSRDLIELRNLALVAELIIRSAMQRR
5982. 4563
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/product-11-aspartate oxidase"
/protein_id="Aspartate"
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DAEFFEGDHALKDIESPERAMLRDEIEATVHQTIQQLPEDLRTALTLREFEGLSYEDI
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VRLYNQNDALPQMAQQGTTPQIALPQVKGPAVLAGYSEEQGAPQVITNSSSSDTRWHE
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/product-"negative regulator for alginate biosynthesis
                                                                                                                                                       /product="conserved hypothetical protein"
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5188. .6138
/genew"mucB"
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/db_xref-"GI:9946651"
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4595. .5179
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/gene≔"algU"
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/gene="mucA"
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Stover,C.K., Pham,X.Q., Erwin,A.L., Mizoguchi,S.D., Warrener,P.,
Hickey,M.J., Brinkman,F.S., Hufnagle,W.O., Kowalik,D.J., Lagrou,M.,
Garber,R.L., Goltry,L., Tolentino,E., Westbrock-Wadman,S., Yuan,Y.,
Smith,K., Spencer,D., Wong,G.K., Wu,Z. and Paulsen,I.T.
Complete genome sequence of Pseudomonas aeruginosa PA01, an
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LRIGLRDASFALRALGIDTPAESGRIARHGDLLAVALGDGRVELWVPAQRAEAVLATL
REHSREAPLDDWLLGQVRAGIGQVFGATRELFIPQMINLQAVGGVSFKKGCYTGGEIV
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LQDDAVADGRISLGSAEGAPLVLLNLPYTLDSDREIQR"
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                                                                       3948 TCCAGGAAGTGAACAAGGATCTCGCCGAGTCCTTCGGCCTCGACAAGCCGTCCGGCGCGC 4007
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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Nature 406 (6799), 959-964 (2000)
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complement(81. .1025)
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/gene="PA0760"
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Gaps

3,

Length 10977;

7155

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AVU30799 2027 bp DNA BCT 31-MAY-1996
Azotobacter vinelandii MucC (mucC) and MucD (mucD) genes, complete
                                                                                                                                                                                                                                                                         TGGTGGCGCAACTGGTGGAAGACGGCCCGGCGGCCAAGGGTGGCCTGCAGGTGGCGATG 7575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tcgtcctcagcctcgacggcggagaaatacgttcttccggcgaccttcccgtcatggtcg 1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae; Azotobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          734 attccggcggcccgctgttcaacttaaaaggacaggtcgtcggcatcaattcgcaaatat 7276 ACTCCGCCGGTCCGCTGCTGAACTGCGGGGGGGGAAGTGGTCGGCATCAACTGCGAAGTGTCGGCATCAACTGCAGATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      teggttegggetteateateageaaaaeggetacateetgaceaataceeaegtegttg
                                                                                                                        ccggtatgggcagtatcaaagtcctgctcaacgacaagcgcgaatataccgccaaactca
                                                                                                                                                                                                               CCGATGCCGACGAGATCCTGGTGCGCCTGTCCGACCGTAGCGAGCACAAGGTTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gootgoccaacgaaagotacacaccottcatccaaaccgacgttgccatcaatccgggca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acagecgcagcggcggattcatgggcatctctttgccatcccgattgacgttgccatga
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                                                                                                                                                                                                                                                     tcggttcggatgtccaatccgatgtcgccttctgaaaatcgacgcaacggaagagctac
                                                                                                                                                                                                                                                                                                                              ccgtcgtcaaaatcggcaatcccaaaaatttgaaaccgggcgaatgggtcgctgccatcg
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Martinez-Salazar,J.M., Moreno,S., Najera,R., Boucher,J.C.,
Espin,G., Soberon-Chavez,G. and Deretic,V.
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                                                               0; Mismatches 244;
                                             5e-58;
                         Score 365.6;
Pred. No. 3.5
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Azotobacter vinelandii
                       26.2%;
68.0%;
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Matches 525;
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KEYWORDS
SOURCE
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AVACSAKSGMGVLEVLERLYUTAIPAPEGEIBAPLQALIIDSMFDNYLGVYSIVRVKNG
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6630..8054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISNDGYILTNNHVVÄDADEILVRLSDRSEHKAKLIGAÖPRSDVAVÜÄIEAÄNLPTLKL
GDSKNLKNGEWUVLAIGSPFGFDBYTAGATGAVSAGKRSELPRRSZYVPFIGTDVAINDGNSG
GPLINLÖGEVVGTNSQIPERSGGFWGLSFAIPIDVALNYADQLKKAGKVSRGWLGVVJ
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VGNMKPGDKILNLDVIRNGQRKSLSMNVGSLPDDDEEILSMGAPGARESSNRLGVYAD
LTAROPRKSLDIOGGVVIREVQDGPAAVIGLRPGDVITHLDNKAVTSTKVFADVAKALP
KNRSVSMRVLRQGRASFITFKLAE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /LEGIS 1 at 10n = "MTLNFPLLLV1AVAVCGALALVDLVLFAPRRAAISSYEGQVNE
PDPAVLEKLKREPLLVEYGKSFFPVLFIVVLRSFLVEPFOIPSGSKFPTLEVGDFIL
WKFAYGIRLPVLDTKV1F1GDPQRGDVWFPRFSEPNINT KRVVGLEGBDTVRYTKE
KRLVVNGELVAAKLYGEEPGTLGSVTLYQEKLGQABHLIREMSRYRIEDDRQWTIPA
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STROKLPDRAMARGOLSIPDLBGLPPWFRDFLERSIPQVPRNRRGQQREAQSLGSGFI
                                                                                                                                                        biosynthesis
                                                                                                                                                      for alginate
VSKRLQTDDGGQMVTVVGEVPLGTAERVALSIRPEAAAQK"
6135. .6590
/gene="mucC"
                                                                                                                                                                                                                                                                                                                                                                                                                         precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="GTP-binding protein LepA"
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                                                                                                                                                        regulator
                                                                                                                                    /transl_table=11
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                                                           'note="PA0765"
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                                                                           6135. .6590
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GPLEDLDGRVIGINSQIFFRSGFRGFISFAIPTEVAMGYADQLKATGKVARGWLGVII
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                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"similar to Photobacterium sp. ORF4 product, encoded by GenBank Accession Number L41667"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      483. .1904
/note="similar to Brucella abortus HtrA protein encoded by
GenBank Accession Number U07352"
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Characterization of the genes coding for the putative sigma factor AlgU and its regulators MucA, MucB, MucC, and MucD in Azotobacter vinelandii and evaluation of their roles in alginate biosynthesis 3. Bacteriol. 178 (7), 1800-1808 (1996)
                                                                                                     2 (bases 1 to 2027)
Martinez-Salazar, J.M., Moreno, S., Najera, R., Boucher, C., Espin, G.
Soberon-Chavez, G. and Deretic, V.
                                                                                                                                                                  Direct Submission
Submitted (30-JUN-1995) Jaime M. Martinez-Salazar, Microbiology,
UTHSCSA, 7703 Floyd Curl Drive, San Antonio, TX 78284, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ttctacgaatttttcaaacgcetcgtcccgaacatgccgaaatcccccaagaagaagca 354
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Pred. No. 2.9e-41;
0; Mismatches 362;
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/product="MucD"
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1. .471
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Chases 1 to 12245)
Simpson.A.J.G., Reinach, F.C., Arruda, P., Abreu, F.A., Acencio, M., Alves, L.M.C., Araya, J.E., Baid.G.S., Haptista, C.S., Barros, M.H., Bonacorsi, E.D., Bordin, S., Bove, J.M., Briones, M.R.S., Bueno, M.R.P., Camargo, A.A., Camargo, L.E.A., Carraro, D.M., Carrer, H., Colauto, N.B., Colombo, C., Costu, F.F., Costa, M.C.R., Costa-Neto, C.M., Coutinho, L.L., Cristofani, M., Dias-Neto, E., Docena, C., El-borry, H., Facincani, A.P., Ferreira, A.J.S.,
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1 (bases 1 to 1215)

2 (bases 1 to 1215)

2 (bases 1 to 1215)

3 (bases 1 to 1215)

4 (bases 1 to 1215)

5 (bases 1 to 1216)

Terenzi, M.L., Siqueira, W.J., de Souza, A.A., de Souza, A.P.,

Terenzi, M.F., Truffi, D., Tsai, S.M., Tsuhako, M.H., Vallada, H., Van
Sluys, M.A., Verjovski-Almeida, S., Vettore, A.L., Zago, M.A., Zatz, M.,

Meidanis, J. and Setubai, J.G.

Xylella fastidiosa Consortium of the Organization for Nucleotide
Sequencing and Analysis, Sao Paulo, Brazil

Nature 406 (6792), 151-157 (2000)
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retietia, V.C.A., Frenco, J.A., Fraga, J.S., Franco, M.C., Fronco, M.C., Gander, E.C., Garnier, M., Goldman, G.H., Goldman, M.H.S., Gomes, S.L., Gruber, A., Ho, P.L., Hohelsel, J.D., Junqueira, M.L., Kemper, E.L., Kitajima, J.P., Krieger, J.E., Kuramae, E.E., Laigret, F., Lambais, M.R., Leite, L.C.C., Lemos, E.G., Lemos, M.V.F., Lopes, S.A., Lopes, C.R., Marchado, J.A., Marchado, M.V., Martins, E.R., Lopes, C.R., Martins, E.R., Marino, C.L., Marques, M.V., Martins, E.A.L., Madeira, H.M.F., Marino, C.L., Marques, M.V., Martins, E.A.L., Martins, E.A.L., Martins, C.Y., Martins, E.C., Martins, C.Y., Monteiro-Vitorello, C.B., Moon, D.H., Nobrega, F.G., Nascimento, A.L.T.O., Netto, L.E.S., Nhani Jr., A., Nobrega, F.G., Nues, L.R., Oliveira, M.A., de Oliveira, M.C., de Oliveira, R.C., Palmieri, D.A., Paris, A. Peirs, A. Peirs, Pereira, G.G., Pereira Jr., H.A., Pesquero, J.B., Quaggio, R.B., Roberto, P.G., Rodriques, V., de M. Rossa, A.J., de Rossa Jr., V.E., de Salva, F.R., da Silva, A.M., Silva, Jr., W.A., da Silva, A.C.R., da Silva, F.R., Truffi, D., Tsai, S.M., Tsubako, M.H., Vallada, H., Van Sluys, M.A., Verjovski-Almeida, S., Vettore, A.L., Zago, M.A., Zatz, M., Meidanis, J. and Setubal, J.C.
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LNODATASEDEDDTAPSKPETSANVELLGLQVENLSAAERBRLASSQNAKGGVRITAV
TAPWARNANPPLVEGLVILRIGRTPVSNVAELNRVLGNYKKGDVIMLLVTNGRGTFYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to GI|1184684 (percent identity: 47 %/query alignment coverage: 91.2 %/subject alignment coverage: 98.9 %); identified by sequence similarity; putative; OFF located using Glimmer/PBSfinder/Start codon shift: -48"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPAPQLVAGLPDFTQLVDQVGPGVVNIETVITRKKVGKRGIPLDNDIPEFFRRFGP
DFQMPNQPRGGQDDEGGIAGRGMGSGFIISKDGYILTNHHVITGASEVTIKLTDRREF
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SALGRSTSDDQRYVPFIQTDVPINQGNSGGPLLNTRGEVIGINSQIFSASGGYMGISF
AIPINLAINAAEQIRKTGKVQRSMLGVEIGPIDALKAQGLGLPDSRGALVNNIPPHSP
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Agene="XF2242"
/notte="hypothetical protein; identified by sequence
similarity; putative; ORF located using Glimmer/RBSfinder"
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Ferreira, V.C.A., Ferro, J.A., Fraga, J.S., Franca, S.C.,
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/protein_id="AAF85040.1"
/db_xref="GI:9107395"
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/protein_id="AAF85041.1"
/db_xref="G1:9107396"
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/organism="Xylella fastidiosa"
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/gene="XF2243"
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REMARK FEATURES

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KKLLEKOKEGKKRRKQIGRVEIPQEAFLAVLQIDNK"
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AVIAAIYLDADLATCRTVVLPWFETALTALPVGKPEKDPKTRLQEWLGARQWSLPVYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to SP|P00803 (percent identity: 40 %/query alignment coverage: 113.5 %/subject alignment coverage: 93.2 %); identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to SP|P43728 (percent identity: 51 %/query alignment coverage: 97.3 %/subject alignment coverage: 96.0 %); identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
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3717. .4517
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4959. .5597
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GTAAAAACAGGCAAAAGTGCAAACGCAGTATGCTCGGTGTGGAAATCGCCCCTATCGACGCAC 1010
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                                                                                                                                                                                                                                                                                                                         CCCACAGGCCGGCCGCCAAAGCAGGGATTGAAGTCGGTGACGTCATCCGCTCAGTGAACG 1130
                                                                                                                                                                                                                                                                                                                                                                                        1131 GCAAAGTAATCAGTAGCTTCAGCGATCTGCCTCCACTGATCGCCATGATGCCGCCAGGCA 1190
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                                                                                                                                                                                                            gtttggcacagtcgttcggtctggataaagccagcggcgttgattgccaaaalccttc
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                                                                                                                               872 aaaacaccggcaaagtccaacgcggacaactgggcgtgattattcaggaagtatcctacg
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Ruelle, J.L.
Basbolls dna and proteins from neisseria meningitidis
Patent: WO 9955872-A 04 -NOV-1999;
RUELLE JEAN LOUIS (BE); SMITHKLINE BEECHAM BIOLOG (BE)
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Sequence 9 from Patent W09955872.
AX011580 GI:9998109
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120 c 102 q
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Neisseria meningitidis
Bacteria; Proteobacteria;
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96.8%;
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KEYWORDS
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                                                                Translation "Mrotverggeravigerbyckstithalvgtkisivsnrpott
Rhrligiatfpeggivlydpeglhregkhpmnrlmnrtargsledvdaallytesthw
Needtlavillidipegppersedtinkidrekgrallpetthinentfttihpysalkr
Kgletlvsdllallpegdpmfsedeitdrsgrflaselvregymrqlgelpyative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATRYVLDPLEGPRRLLSEHNNAKRRDTATGHVLLALARNQIPNTNDLAGLRRSMRAVL
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/db_xref="GI:9107402"
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           /product="GTP binding pro
/protein_id="AAF85046.1"
/db_xref="G1:9107401"
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Submitted (16-MAY-2000) Department of Medicine and Genetics, University of Washington,
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ELRVGDYALAIGNPFGLGGTVTSGIVSALGRSGLNIENLENTIQTDAAINSGNSGGAL
LNLEGELIGINTALLGPNGGVTGIGFAIPSNMVRDLESQIVKYGEVRRGQLGIGTEL
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MGANKQVALGLIRDGKEQTVKVTLKKADDSFILASALHPALEGAKLGTTSEPVSGVAV
SEIDPRSPAAASGLQKGDVIIGVNRLRINSLEELSKALKNKPDVLALNIQRGDSSLYL
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Lin.T.-N., Lin,T.-J. and Liou,C.-M.
Direct Submission
Submitted (07-AUG-2000) Agricultural Chemistry, National Taiwan
University, No.1 Rosesvelt Road Section 4, Taipei 106, Taiwan
Location/Qualifiers
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Aeromonas hydrophila htrA-like serine protease (prtS1) gene,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 246; DB 2; Length 13
Pred. No. 6.4e-36;
0; Mismatches 330; Indels
241 AGGCGGGCGACGAAATTCTTGCCGTC-GGGCAAGTCCCCGTCAA 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .1362
/organism="Aeromonas hydrophila"
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                                                                                                                                                                                                                                                                                                                                                                           prtS1
                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 1362)
Lin,T.-N., Lin,T.-J. and Liou,C.-M.
Aeromonas hydrophila strain CKH-29
                                                                                                                                                                                                                                                                                             gamma
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                                                                                                                                                                                                                                                                                         Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="prtS1"
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                                                                                                                                                                                                     AF293977.1 GI:9945003
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58.3%;
                                                                                                                                                                                                                                                  Aeromonas hydrophila.
                                                                                                                                                                                                                                                                      hydrophila
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Best Local Similarity 58.3
Matches 470; Conservative
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                                                                                                                                                                   complete cds.
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                                                                                                                                                                                                                                                                      Aeromonas l
Bacteria; 1
                                                                                                                                                                                                                                                                                                                 Aeromonas.
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ORIGIN
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TITLE
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AUTHORS
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KEYWORDS
SOURCE
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GRAPSLEDGFKTLYPLDVLASAGLRPQGPLGGHRQASLLRLDMGRNYQYWYGLPNFYV
ITRYNHSTHYAMAVWELGKEVDRVRHRSVVRQD"
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ESSLGSAVIMSAEGYLLTNNHVTAGADQIIVALRDGRETIAQLYGSDPETDLAVLKID
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DAAINDFNSGGALVDAAGNIIGINPALFSKSGGSGG1GRAIPTKLALEVYGSITERGO
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Location/Qualifiers
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VDPDSDAGDRGLKEGEKIVSVNNORPNRQTTFSR"

18 a 626 c 626 g 344 L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria: Proteobacteria: alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Sinorhizobium.

(bases 1 to 1974)

(clazebrook,J., Ichige,A. and Walker,G.C.

Genetic analysis of Rhizobium meliloti bacA-phoA fusion results in identification of degp: two loci required for symbiosis are closely linked to degp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (12-JUL-1995) Jane Glazebrook, Department of Molecular
Biology, Massachusetts General Hospital, Wellman 10, MGH, Boston,
gaagaaatcacaatcaaagccaagctgggc--aacgccgccgagcataccggcgcatcat 1201
                                                                                                                                                           376 ggttcgggcttcatcatcatcagcaaaacggctacatcctgaccaatacccacgtcgttgcc 435
                                                                                                                                                                                                                                                                                                         Activation 2 1974 bp DNA BCT 05-MAR-1996
Rhizobium meliloti RmDEGP (degP) gene, complete cds.
U31512
U31512.1 GI:951169
                                                             gtcatggtcggcgccattacgccgggaaaagaagtcagcctcggcgtatggcgcaaaggc
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Best Local Similarity 53.4%; Pred. No. 9.4e-30;
Matches 539; Conservative 0; Mismatches 461
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236. 1690
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Glazebrook, J.
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VERSION
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AUTHORS
TITLE
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REFERENCE
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JOURNAL
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Pred. No. 7.7e-31;
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llarity 55.9%;
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475; Conserv
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Matches 47
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643	436	495 763	555 823	615 883	675 943	735	795	855 1123	915 1183	975 1243	1035	1095	1155	1212	1272	1329
q	Qy Db	Oy Db	Qy Db	oy op	Qy Dp	Oy Dp	oy Ob	Oy Dp	Qy Db	Qy Dp	oy ob	Oy Dp	Qy Op	oy ob	Qy	Oy Dp

Search completed: March 22, 2001, 04:06:30 Job time: 4575 sec

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(ANTE-) ANTEX BIOLOGICS INC.
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P-PSDB; Y83150.
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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The NGSP polypeptide of N. gonorrhoeae has conserved Arg-Gly-Asp and Arg-Gly-Asn motifs near the C-terminus which function as adherence domains for extracellular matrix proteins. Using the NGSP polypeptide as a vaccine produces antibodies which inhibit binding of N. gonorrhoeae to the host's cellular matrix reducing attachment and/or subsequent invasion. The NGSP polypeptide and its peptide fragments can be used to immunise an animal and produce an immune response. They can also be used as ligands to detect antibodies elicited in response to Neisseria infections and also as antigens or immunogens for inducing Neisseria-specific antibodies which are useful in response to detect Neisseria in biological specimens. Nucleotides encoding NGSP or its fragments can be used as probes to identify Neisseria in biological specimens by hybridization or polymerase chair reaction amplification. The NGSP polypeptide can also be used in screening assays to identify agents and compounds which useful as diagnostic, prophylactic or therapeutic agents against Neisseria
                        from
Neisseria
                      NGSP polypeptide and polynucleotide sequence ul for diagnosis, prevention or treatment of
                                                                                                                  60-61; 68pp; English.
                      Non-cytosolic NGS
Neisseria useful
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                                                                     infections
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Sequence 1395 BP; 359 A; 438 C; 353 G; 245 T; 0 other;

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                                gccaaaggcagaagcctgcccaacgaaagctacacacccttcatccaaaccgacgttgcc
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The present sequence is a DNA encoding Neisseria meningitidis NNASP protein. NNASP is a non-cytosolic protein, with antibacterial and antilnflammatory activity. It shows sequence similarity to E. ooli Degp (HtrA) protein. NNASP proteins can be used as ligands to detect anti-NNASP antibodies elotited in response to N. meningitidis infections. Cytotoxic anti-NNASP antibodies can be used as vaccines. NNASP proteins and DNA may be used for diagnosis, therapy or prophylaxis of Neisserial infections such as, bacterial meningitidis and septicaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aa: gqvpvndeagfrkamdkagk
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                                                                                                      // Inote= "Does not include stop codon" / transl_except= (pos:22..24, aa:Leu) / transl_except= (pos:49..51, aa:Ser) / transl_except= (pos:64..66, aa:Asp) / transl_except= (pos:124..126, aa:Lys) / transl_except= (pos:127..174, aa:Val) / transl_except= (pos:172..174, aa:Val) / transl_except= (pos:400..402, aa:Lys) / transl_except= (pos:400..402, aa:Asp) / transl_except= (pos:649..654, aa:Thr) / transl_except= (pos:649..654, aa:Gly) / transl_except= (pos:964..966, aa:Gly) / transl_except= (pos:1162..1164, aa:Gly) / transl_except= (pos:1162..1164, aa:Gly) / transl_except= (pos:1189..1191, aa:Ile) / transl_except= (pos:1300..1302, aa:Gly) / transl_except= (pos:1300..1302, aa:Gly) / transl_except= (pos:1374..1356, aa:Gly) / transl_except= (pos:1374..1356, aa:Gly) / transl_except= (pos:1378..1356, aa:Gly) / transl_except= (pos:13788..1356, aa:Gly) / transl_except= 
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P-PSDB; Y70413.
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Score 1393.4;
Pred. No. 0;
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99.9%;
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253015 to 254536, 254577 to 254615, and Y74253 to Y75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. 254537 to 254576 and 254616 to 255473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of immunogenic compositions. The polypeptides can be used in the annufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
gcaggcattaccettcagacacataccgacagcagcggcaaacacctcgtcgtcgtacgg 1320
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Scarselli
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Scalato E,
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Rappuoli R,
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, Pizza M, R
, Venter JC;
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Petersen J,
Tettelin H,
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02-SEP-1998;
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caggoggagacatcgtcctcagcctcgacggcggagaaatacgtcttccggcgacctt
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The present sequence is a DNA encoding Neisseria meningitidis NMASP protein. NNASP is a non-cytosolic protein, with antibacterial and antiinflammatory activity. It shows sequence similarity to E. coli DegP (HtrA) protein. NMASP proteins can be used as ligands to detect anti-NMASP antibodies elocited in response to N. meningitidis infections. Cytotoxic anti-NMASP antibodies can be used as vaccines. NMASP proteins and DNA may be used for diagnosis, therapy or prophylaxis of Neisserial infections such as, bacterial meningitidis and septicaemia.
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                                                                                                                                                                                     Neisseria meningitidis NMASP polypeptide, nucleotide sequences and antibodies, useful in vaccines against infection
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99.9%; Pred. No. 0;
iive 0; Mismatches
                                                                                                                                                                                                                                               75pp; English.
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98US-0098685
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Best Local Similarity 99.9
Matches 1325; Conservative
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                                                                                                                                    gcattgattgccaaaatccttcccggcagccccgcagaacgtgccggcctgcaggcgggc 1029
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                         agaagcctgcccaacgaaagctacacacttcatccaaaccgacgttgccatcaatccg
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                                                                  atatacagccgcagcggcggattcatgggcatctcctttgccatcccgattgacgttgcc
                                                                               gtcggcgccattacgccgggaaaagaagtcagcctcggcgtatggcgcaaaggcgaagaa
                                                                                                         attattcaggaagtatcctacggtttggcacagtcgttcggtctggataaagccagcggc
            601 agaagcctgcccaacgaaagctacacaccttcatccaaaccgacgttgccatcaatccg
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The present sequence encodes a BASB013 polypeptide isolated from
Neisseria meningitidis. BASB013 polynucleotides and polypeptides may be
employed as research reagents and material for the discovery of
treatments and diagnostics for diseases, particularly human discascs.

They can be used for diagnosis of disease, staging of disease, or
determining response of an infectious organism to drugs. The
polypeptides may be used as a source for hybridisation probes, and
for screening of genetic mutations, serotype, organism or strain
identification, identification of mutation in BASB013 sequences, and as
components of arrays which are useful for diagnostic and prognostic
purposes. The polypeptides can be used to produce antibodies. The
polypeptides can also be used in vaccine formulations, and to identify
agonists and antagonists. The polypeptides, antibodies, agonists and
antagonists which are bacteristatic) are used for the treatment and
prevention of diseases such as upper respiratory tract infection,
invasive bacterial diseases such as bacteraemia and meningitis, and for
the development and screening of antibacterial drugs. They are also used
in the prevention of adhesion of bacterial to eukaryotic matrix proteins
on in-dwelling devices, or to extracellular proteins of
thus prevent tissue damage and/or block the normal progression of
pathogenesis in infections initiated other than by the implantation of
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                                                                                                                                                                                                                                                                                                                                                                                    prepare vaccines against bacterial infections
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                                                                                                                       (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Page 78-79; 94pp; English.
99WO-EP02765
                                                           98GB-0008734
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P-PSDB; Y52995.
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Matches 1355; Conserv
20-APR-1999;
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Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy; ds.

Neisseria meringitidis

W09957280-A2

Neisseria meningitidis ORF 986 partial DNA sequence SEQ ID NO:2969

(first entry)

21-MAR-2000

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09-OCT-1998;
09-OCT-1998;
25-FEB-1999;
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02-SEP-1998;
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Hickey | Ratti (

G, R,

Grandi G, Rappuoli F

Pizza M, Venter JC; Galeotti C,

Petersen J, Tettelin H,

ပဲ Fraser 2000-062150/05

WPI; 2000-06215 P-PSDB; Y75749.

GENOMIC RES

(CHIR ) CHIRON (GENO-) INST GE

980S-0094869-980S-0098994-980S-0099062-980S-0103794-980S-0103794-980S-0103796-990S-0121528-

09-0CT-1998;

99WO-US09346

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11-NOV-11999

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                                                                                                                                                               novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. 24537 to 254576 and 224616 to 255473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of immunogenic compositions. The polypeptides and compositions of medicaments for treating or preventing infection due to Neisserial bacteria decria, or to raise antibodies. They may also presence of Neisseria bacteria, or to raise antibodies. They may also he used to screen for agonists or antagonists, which may themselves have use as antibocterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
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Novel Neisserial polypeptides predicted to be useful antigens vaccines and diagnostics \boldsymbol{\cdot}
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Pred. No. 0;
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Matches 1352; Conservative
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09-OCT-1998;
25-FEB-1999;
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253015 to 254536, 254577 to 254615, and Y74253 to Y75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. 254577 to 254576 and 254616 to 255473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; Infection; meningitis; septicaemia; antibacterial; gene therapy; ds.
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Scarselli
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Rappuoli R,
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98US-0094869.
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                        44; Indels
       other;
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                  DB
       Ξ,
                 Score 1313.8;
Pred. No. 0;
0; Mismatches
       G; 265
protocols
       382 A; 469 C; 382
gene therapy
                 Query Match
Best Local Similarity 96.8%;
Matches 1350; Conservative
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       BP;
       Sequence 1500
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                                                                                                                                                                                                                                                                                                                                                                      nucleotide sequence
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gecageggegeattgecaaaateetteeeggeageeeegeagaaegtgeeggeetg
       meningitis
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it bacterial infections -
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the development and screening of antibacterial drugs. They are also used in the prevention of adhesion of bacteria to eukaryotic matrix proteins on in-dwelling devices, or to extracellular proteins on wounds, and to thus prevent tissue damage and/or block the normal progression of pathogenesis in infections initiated other than by the implantation of They can be used for diagnosis of disease, staging of disease, or determining response of an infectious organism to drugs. The polynucleotides may be used as a source for hybridisation probes, and for screening of genetic mutations, serotype, organism or strain identification, identification of mutation in BASB013 sequences, and as components of arrays which are useful for diagnostic and prognostic purposes. The polypeptides can be used to produce antibodies. The polypeptides can also be used in vaccine formulations, and to identify antagonists (which are bacteristatic) are used for the treatment and prevention of diseases such as upper respiratory tract infection, invasive bacterial diseases such as bacteraemia and meningitis, and for in-dwelling devices or by other surgical techniques. 

Sequence 1500 BP; 370 A; 469 C; 392 G; 269 T; 0 other;

ä 240 300 360 540 180 180 300 360 420 420 480 480 009 600 gccaaaggcagaagcctgcccaacgaaagctacacccttcatccaaaccgacgttgcc 720 9 9 Gaps tgcgaaaaggcaggcagctttttcggtgcggacaaaaaagaagcatccttcgtagaacgc aacggcagcggcaatgccgaaaccgattccgacccgcttgccgacagcgacccgttctac ggcggattgaacttcggttcgggcttcatcatcagcaaaaacggctacatcctgaccaat ggcggattgaacttcggttcgggcttcatcatcagcaaagacggctatttctgaccaat acccacgtcgttgccggtatgggcagtatcaaagtcctgctcaacgacaagcgcgaatat acgcacgtcgttaccggcatgggcagtatcaaagtcctgctcaacgacaagcgcgaatat gtcgccgccatcggcgcccttcggcttcgacaacagcgtgaccgccggcatcgtgtcc gccaaaggcagaagcctgcccaacgaaagctacacaccttcatccaaaaccgacgttgcc atcgaacaccaaaagacgacggcagtgtcagtatgctgctgcccgactttgcccaactg gttcaaagcgaaggcccggcagtcgtcaatattcaggcagccccggccccgag aacggcagcggcaatgccgaaaccgattccgacccgcttgccgacagcgacccgttctac acggaagagctacccgtcgtcaaaatcggcaatcccaaaaatttgaaaaccgggcgaatgg gtcgctgccatcggcgcgcccttcggctttgacaacagcgtgaccgccggcatcgtgtcc 1; Length 1500; Indels 21; 75; DB Score 1263; D Pred. No. 0; 0; Mismatches 90.5%; 94.6%; Conservative Query Match Best Local Similarity Matches 1319; Conserv 61 61 121 121 181 181 241 241 301 361 421 481 481 541 541 601 601 199 301 361 421 199 Q 6 QQ g g q ò g g g 8 à g ò ò ò ò à ò à ò

Neisseria meningitidis; BASB013; diagnosis; infection; vaccine; antibiotic; upper respiratory tract infection; bacteraemia; meningitis; invasive bacterial disease; antibacterial; ss. 1379 900 gccagcggcgcattgattgccaaaatccttcccggcagccccgcagaacgtgccygcctg 1201 tecaaaacagatgaageeeetacaeegaacageaateeggtaegtteteggtegatee 1201 tecaaaaeeggteegateeteggtegataegtteteggtegataeeee atcaatccgggcaattccggccggccgctgttcaacttaaaaggacaggtcgtcggcatc gacgttgccatgaatgtcgccgaacagctgaaaaacaccggcaaagtccaacgcggacaa gacgttgccatgaatgtcgccgaacagctgaaaaacaccggcaaagtccaacgcggacaa 961. gccggcggcgcactgattgccaaaatcctgcccggcagcccgcagaacgtgccggcctg caggogggggacatcgtcctcagcctcgacggcggagaaatacgttcttccggcgacctt cccgtcatggtcggcgccattacgccgggaaaagaagtcagcctcggcgtatggcgcaaa ggcgaagaaatcacaatcaaagccaagctgggcaacgccgagcatacteatca gcaggcattacccttcagacacataccgacagcagcaggcaaacacctcgtcgtacgg 1261 gcaggcattaccettcagacacataccgacagcagcggcggacggcttgtcgtcgtggg 1141 ggtaaggaaatcaccgttgccgtcaaactgggcaatgcttccgaacaaaccggttcctcg gtttccgacgcggcagaacgcgcaggcttaaggcacggcgacgaaatcctagccgtcagg Neisseria meningitidis strain ATCC 13090 BASB013 nucleotide ВЪ 98GB-0008734 99WO-EP02765 233305 standard; DNA; 1500 (first entry) 1381 gcaagtccccgtcaa 1395 1380 gcaagtccccgtcaa 1394 Neisseria meningitidis 21-FEB-2000 W09955872-A1 20-APR-1999; 23-APR-1998; 04 - NOV - 1999 1021 1021 1081 1081 1141 1261 1321 901 721 961 901 RESULT Z33305 g Ob Q g qq g QQ g q g g ò ò οy ογ ò ò οy ò ò ò ò

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The present sequence encodes a BASB013 polypeptide isolated from Neisseria meningitidis. BASB013 polynucleotides and polypeptides may be employed as research reagents and material for the discovery of treatments and diagnostics for diseases, particularly human diseases. They can be used for diagnosts of disease, staging of disease, or determining response of an infectious organism to drugs. The polynucleotides may be used as a source for hybridisation probes, and for screening of genetic mutations, serotype, organism or strain identification of mutation in BASB013 sequences, and identification of mutation in BASB013 sequences, and as components of arrays which are useful for diagnostic and prognostic purposes. The polypeptides can be used to produce antibodies. The polypeptides can be used to produce antibodies. The polypeptides can be used to produce antibodies. Agonists and antagonists. The polypeptides, antibodies, agonists and antagonists. The polypeptides, antibodies, agonists and antagonists. The polypeptides, antibodies, agonists and antagonists and assuch as bacteratedry tract infection, the dared correction diseases such as bacteraemia and meningitis, and produce the dared correction and decreases and an eningitis, and antibodies.
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                                                                                                                                                                                                                polypeptides from Neisseria meningitis used t bacterial infections
                        SMITHKLINE BEECHAM BIOLOGICALS.
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Sequence 1500 BP; 370 A; 468 C; 393 G; 269 T; 0 other;

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   DB 21; Length 1500;
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Score 1258.2;
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The NGSP polypeptide of N. gonorrhoeae has conserved Arg-Gly-Asp and Arg-Gly-Asn motifs near the C-terminus which function as adherence domains for extracellular matrix proteins. Using the NGSP polypeptide as a vaccine produces antibodies which inhibit binding of N. Gonorrhoeae to the host's cellular matrix reducing attachment and/or subsequent invasion. The NGSP polypeptide and its peptide fragments can be used to immunise an animal and produce an immune response. They can also be used as ligands to detect antibodies elicited in response to Neisseria infections and also as antigens or immunogens for inducting Neisseria-specific antibodies which are useful in immunoassays to detect Neisseria in biological specimens. Nucleotides encoding NGSP or its fragments can be used as probes to identify Neisseria in biological specimens by hybridization or polymerase chair reaction amplification. The NGSP polypeptide can also be used in screening assays to identify agents and compounds which useful as diagnostic, prophylactic or therapeutic agents against Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            n-cytosolic NGSP polypeptide and polynucleotide sequence from isseria useful for diagnosis, prevention or treatment of Neisseria
                                                                 NGSP; polypeptide; peptide; vaccine; immune response; antibody; cellular matrix; adherence domain; ligand; detection; diagnosis; screening; probe; primer; prophylaxis; therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is a DNA encoding Neisseria meningitidis NMASP protein. NNASP is a non-cytosolic protein, with antibacterial and antilnflammatory activity. It shows sequence similarity to E. coli Degp (HtrA) protein. NMASP proteins can be used as ligands to detect antibodies elicited in response to N. meningitidis infections. Cytotoxic anti-NMASP antibodies can be used as vaccines. MASP proteins and DNA may be used for diagnosis, therapy or prophylaxis of Neisserial infections such as, bacterial meningitidis and septicaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09
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                                                                                                                                  cytotoxic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sednences
                                                                                                                                 NMASP; non-cytosolic; antibacterial; antiinflammatory; cytotox
anti-NMASP antibody; vaccine; diagnosis; therapy; prophylaxis;
Neisserial infection; meningitidis; septicaemia; ds.
                                                                                                                                                                                                                                                    /product= "Neisseria meningitidis protein"
/transl_except= (pos:499..501, aa: Xaa)
/note= "Xaa is unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein sequence represented in SEQ ID NO:2 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1347 BP; 338 A; 428 C; 344 G; 236 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis NMASP polypeptide, nucleotide antibodies, useful in vaccines against infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
                                                                                                        Neisseria meningitidis NMASP protein-1 encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1176.2;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75pp; English.
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ilarity 97.2%;
Conservative C
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                                                                                                                                                                                                                                                                                                                                                                                        98US-0098685
                           Z51533 standard; DNA; 1347
                                                                                                                                                                                                                             1..1347
/*tag= a
                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                  BIOLOGICS
                                                                                                                                                                                                                                                                                                                                                                                                                                            Harris AM;
                                                                                                                                                                                      Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000-256581/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 41; Page 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 1207; Conserv
                                                                                                                                                                                                                                                                                                            WO200012535-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                   (ANTE-) ANTEX
                                                                                                                                                                                                                                                                                                                                                                                        01-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                              01-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Jackson WJ,
                                                                               03-JUL-2000
                                                                                                                                                                                                                                                                                                                                    09-MAR-2000
                                                                                                                                 NMASP; non-
anti-NMASP
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1080

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The present sequence encodes a conserved BASB013-C polypeptide isolated from Neisseria meningitidis. BASB013 polynucleotides and polypeptides may be employed as research reagents and material for the discovery of treatments and diagnostics for diseases, staging of diseases, or determining response of an infectious organism to drugs. The copynucleotides may be used as a source for hybridisation probes, and polynucleotides may be used as a source for hybridisation probes, and for screening of genetic mutations, serotype, organism or strain identification, identification of mutation in BASB013 sequences, and as components of arrays which are useful for diagnostic and prognostic purposes. The polypeptides can be used to produce antibodies. The polypeptides can also be used in vaccine formulations, and to identify agonists and antagonists. The polypeptides, antibodies, agonists and antagonists and supper tespiratory tract infection.

Invasive bacterial diseases such as upper respiratory tract infection, invasive bacterial diseases such as bacterial drugs. They are also used in the prevention of adhesion of bacterial or eukaryotic matrix proteins on in-dwelling devices, or to extracellular proteins on wounds, and to thus prevent tissue damage and/or block the normal progression of pathogenesis in infections in intentiated other than by the implantation of
                                                                                                                                                                                      Nelsseria meningitidis; BASB013; diagnosis; infection; vaccine; antibiotic; upper respiratory tract infection; bacteraemia; meningitis; invasive bacterial disease; antibacterial; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polynucleotides and polypeptides from Neisseria meningitis used to prepare vaccines against bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1110 BP; 280 A; 350 C; 279 G; 201 T; 0 other;
                                                                                                                                               nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in-dwelling devices or by other surgical techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page 81; 94pp; English.
                                                                                                                                               Neisseria meningitidis BASB013-C
                           BP.
                                                                                                                                                                                                                                                                                                                                                                                             99WO-EP02765.
                                                                                                                                                                                                                                                                                                                                                                                                                                     98GB-0008734
                         233308 standard; DNA; 1110
                                                                                                       (first entry)
                                                                                                                                                                                                                                                                        Neisseria meningitidis.
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                                                                                                                                                                                                                                                                                                                                                                                             20-APR-1999;
                                                                                                       21-FEB-2000
                                                                                                                                                                                                                                                                                                                                                    04-NOV-1999
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242 acggcagcggcaatgccgaaaacgattccgacccgattgccgacaacgacccgttctacg
                                                                                                                                          302 aatttttcaaacgcctcgtcccgaacatgcccgaaatcccccaagaagaagcagatgacg
                                                                                                                                                                                         geggattgaactteggttegggetteateateageaaaaeggetaeateetgaeeaata
                     tegaacacaccaaagacgacggcagcgtcagtatgetgetgecegaetttgcccaaets,
                                                                                            242 acggcagcgacaatgccgaaaccgattccgacccgcttgccgacagcgacccgtt.ctacg
togaacacacaaagacgacggcagtgtcagtatgctgctgcccgactttgcccaact
                                                                                                         ccgtcatggtcggccattacgccggga 1110
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                    122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tgttcaaaaaataccaatacttcgctttggcggcactgtgtgccgccttgctggcaggct 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tgttcaaaaaataccaatacctcgctttggcagcactgtgtcgccgcctcgctggcaggct 61
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ccagcggcgcattgattgccaaaatccttcccggcagcccgcagaacgtgccggcctgc 1021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1022 aggogggegacatcgtcctcagcctcgacggcggagaaatacgttcttccgggcgaccttc 1081
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421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    842 acgttgccatgaatgtcgccgaacagctgaaaaacaccggcaaagtccaacgguacaac 901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    961
                                                                                                                           782 attcgcaaatatacagccgcagcggcggattcatgggcatctcctttgccatcccgattg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aggcgggcgacatcgtcctcagcctcgacggcggagaaatacgttcttccggcgaccttc
                                        422 cccacqtcqttgccggtatgggcagtatcaaagtcctgctcaacgacaagcgcgaatata
                                                               cggaagagctacccgtcgtcaaaatcggcaatcccaaaaatttgaaaccgggcgaatggg
                                                                                                                                                                                                                                                            542 cggaagagctgcccgtcgtcaaaatcggcaatcccaaagatttgaaaccgggcgaatggg
                                                                                                                                                                                                                                                                                                       tcgctgccatcggcgcgcccttcggctttgacaacagcgtgaccgccggcatcgttccg
                                                                                                                                                                                                                                                                                                                                               602 tegeegecateggegegectteggettegacaacagegtgacegeeggeategtgteeg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tcaatccgggcaattccggcggcccgctgttcaacttaaaaggacaggtcgtcggcatca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           782 actogoaaatatacagocgocagoggoggattoatggggcatttoottogocatocogattg
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62 62

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The present sequence encodes a variable BASB013-V polypeptide isolated
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                                                                                                                                                                                                                                                                                                                                       The present sequence represents a Pseudomonas aeruginosa nucleic aicd sequence. P. aeruginosa is an opportunistic human pathogen present in soil water and plants. The specification describes virulence polypeptides and nucleic acid sequence encoding such polypeptides. These sequences can be used to identify a compound which is capable of decreasing the expression of a pathogenic virulence factor. Compounds that inhibit the expression or activity of virulence factor polypeptides can be used to treat pathogenic infections, especially where the infection is a P, seruginosa infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                         note: the sequences given in the specification were poorly legible, and in some instances assumptions were made as to the identity of the base; it is therefore possible that the sequence given below is not entirely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           teggegeggaccegegeagegaegtggeggtgetgaagategagg---egaagaacetge 522
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                                                                                                                                                                                                                                         Mahajan-Miklos
                                                                      Human pathogen; virulence polypeptide; virulence factor; pathogenic infection; Pseudomonas aeruginosa infection; ss
                                                                                                                                                                                                                                                                                                  Virulence factors useful in developing disease treatments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP; 267 A; 461 C; 471 G; 237 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 277;
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                                                                                                                                                                                                                                            HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 364.8;
                                                  Nucleotide sequence of the PA14 degP gene
                                                                                                                                                                                                                                             Goodman
                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 27; 228pp; English
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66.0%;
                                                                                                                                                                                                                                             Drenkard
Tsongalis
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                                                                                                                                                                                                 97US-0066517
                               (first entry)
                                                                                                                                                                                                                      (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 66.0
Les 544; Conservative
                                                                                                            Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                             WPI; 1999-357851/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                             Cao H,
                                                                                                                                                                                                                                                       Tan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1436
                                                                                                                                                                            25-NOV-1998;
                                                                                                                                                                                                 25-NOV-1997;
                               25-OCT-1999
                                                                                                                                 WO9927129-A1
                                                                                                                                                       03-JUN-1999
                                                                                                                                                                                                                                                          Rahme LG,
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Neisseria meningitidis; BASB013; diagnosis; infection; vaccine; antibiotic; upper respiratory tract infection; bacteraemia; meningitis; invasive bacterial disease; antibacterial; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tocaggaagtgaacaaggatetegeegagteetteggeetegacaageegteeggegege 942
                                                                                                                             762
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                                                                                                                                                                                                                                                                                                                                                                                     ttcaggaagtatcctacggtttggcacagtcgttcggtctggataaagccagcggcat
attcoggcggccgctgttcaacttaaaggacaggtcgtcggcatcaattcgcaaatat
                                                                                                     acagccgcagcggcggattcatgggcatctcctttgccatcccgattgacgttgccatga
                                                                                                                                                                                                       atgtcgccyaacagctgaaaaacaccggcaaagtccaacgcggacaactgggcgtgatta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1154 caatcaaagccaagctgggcaacgccgccgagcataccggcgca 1197
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from Neisseria meningitidis. BASB013 polynucleotides and polypeptides
may be employed as research reagents and material for the discovery of
treatments and diagnostics for diseases, particularly human diseases.
They can be used for diagnosis of disease, staging of disease, or
determining response of an infectious organism to drugs. The
components of genetic mutations, serotype, organism or strain
identification of mutation in BASB013 sequences, and
identification of mutation in BASB013 sequences, and
components of arrays which are useful for diagnostic and prognostic
pulposes. The polypeptides can be used in vaccine formulations, and to identify
agonists and antagonists. The polypeptides, antibodies, agonists and
antagonists which are bacteristatic) are used for the treatment and
antagonists (which are bacteristatic) are used for the treatment and
component and screening of antibacterial drugs. They are also used
the development and screening of antibacterial drugs. They are also used
the development than development of adheston of bacterial or eukaryotic matrix proteins
on in-dwelling devices, or to extracellular proteins on wounds, and to
thus prevent tissue damage and/or block the normal progression of
the pethogenesis in infections initiated other than by the implantation of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1111 aaagaagtcagcctcggcgtatggcgcaaaggcgaagaaatcacaatcaaagccaagctg 1170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS-1; presentlin; presentlin-1; PSP-1; Alzheimer's disease; htrA; serine protease; neurodegeneration; predisposition; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ı,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 21; Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 18.7%; Score 260.2; DB 21; Length Best Local Similarity 96.8%; Pred. No. 2.8e-61; Matches 276; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in-dwelling devices or by other surgical techniques.
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 390 BP; 106 A; 120 C; 102 G; 62 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product- htrA serine protease
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199..1674
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The sequence is that encoding the serine protease htrA which was used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          622 ttcggctttgacaacagcgtgaccgccggcatcgtgtccgccaaag---gcagaagcctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          787 tttggtctgggcgagacggtaacttccgggattgtctctgcgctggggcgtagcggcctg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1854;
                                                                                                                                                                                                                                                                         Nucleic acids encoding human serum protease protein(s) - used diagnosing pre-disposition to {\sf Alzheimer}{}'s disease, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 386; Indels
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                                                                                                                                                                         Karran EH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.6%; Score 176.4; DB 1 52.0%; Pred. No. 2.4e-38;
                                                                                                                                                                       Clinkenbeard HE, Creasy CL,
                                                                                                                                                                                                                                                                                                                           Example 2; Page 27-28; 65pp; English
                                                                                                                   (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                97EP-0306501
                                                 96US-0032875
                                                                  96US-0025436
96US-0027873
                                                                                                                                                                                                                                                                                                                                                                             in the isolation of PSP1.
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                26-AUG-1997;
                                                13-DEC-1996;
06-SEP-1996;
                                                                                  25-OCT-1996;
                                                                                                                                                                     Browne MJ,
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1147 agccaggtLctgcctaattcctccgctgcaaaagcgggcattaaagcgggtgatgtgatc 1206
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Sequence 3, Appli Sequence 28, Appl Sequence 26, Appl Sequence 2, Appli Patent No. 5248599

Sequence

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Sequence 2 Sequence 5 Sequence 5

Sequence 1, A Sequence 1, A Sequence 1, A Sequence 8, A Sequence 8, A Sequence 1, A

US-08-923-454A-24
US-08-923-454A-30
US-08-923-454A-3
US-08-923-454A-3
US-08-923-454A-2
US-08-923-454A-2
US-08-923-454A-2
US-08-923-454A-2
US-08-923-454A-2
US-08-923-454A-2
US-08-953-168C-1
US-08-953-168C-1
US-08-963-168C-2

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GENERAL INFORMATION:
APPLICANT: Creasy, Caretha
APPLICANT: Livi, George
APPLICANT: Karran, Eric
APPLICANT: Clinkenbeard, Helen
APPLICANT: Southan, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beecham Corporation
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APPLICATION NUMBER: US/08/923,454A
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1
10S-08-20344A-13
Sequence 13, Application US/08923454A
Patent No. 6004794
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FastSEQ Version 1.5
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STREET: 709 Swedeland
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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CITY: King of Prussia
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STRANDEDNESS: single
TOPOLOGY: linear
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-350-741-1
US-08-463-85A-1
US-08-463-85A-1
US-08-474-499-7
US-08-307-279A-7
PCT-US95-06211-7
US-08-483-859-1
US-08-483-859-1
US-08-487-167-1
US-08-482-816-1
US-08-826-149-1
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Maximum Match 100%
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; LOCATION:
US-08-350-741-1
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                                                                12.6%; Score 176.4; DB 3; 52.0%; Pred. No. 1.5e-39; ive 0; Mismatches 386;
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Patent No. 5804194
GENERAL INFORMATION:
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APPLICANT: CHARLES I.G.,
APPLICANT: HORMAECHE C.E.,
APPLICANT: JOHNSON K.S.,
                                                                                        Best Local Similarity 52.0 Matches 421; Conservative
JS-08-923-454A-13
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APPLICATION NUMBER: US/08/350,741
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52.6%; Pred. No. 2.6e-39;
tive 0; Mismatches 364
                                                                                          STREET: 8th FLOOR, 1100 NORTH GLEBE ROAD CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 30-MAR-1990
APPLICATION NUMBER: PCT/GB91/00484
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 117-158
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952,737
FILING DATE: 09-MAY-1994
APPLICATION NUMBER: US 07/952,737
FILING DATE: 30-MOY-1992
APPLICATION NUMBER: GB 9007194.5
FILING DATE: 30-MAR-1990
                                                                           ADDRESSEE: NIXON and VANDERHYE PC
                                                                                                                                                                                                                                                                        IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
TITLE OF INVENTION: LIVE VACCINES NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPAONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELES: 200797 NIXN UR
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
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STRANDEDNESS: double
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ccettcatccaaaacgacgttgccatcaatccgggcaattccggcggccgctgttcaac 756
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                                                          ttaaaaaggacaggtcgtcggcatcaattcgcaaatatacagccgccggcggcggattcatg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: CHARLES, Ian G.
APPLICANT: HORMAECHE, CATLOS E.
APPLICANT: HORMAECHE, CATLOS E.
APPLICANT: CHATFIELD, STEWEN N.
TITLE OF INVENTION: LIVE VACCINES
NUMBER OF SEQUENCES:
ADDRESSEE: NIXON and VANDERHYE PC
STREET: 81h FLOOR, 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/463,875A FILING DATE: 05-JUN 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/340,741
FILING DATE: 07-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UMBER: US 07/952,737
30-NOV-1992
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REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 117-158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER. IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
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FILING DATE: 30-NOV
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CITY: ARLINGTON
STATE: VIRGINIA
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APPLICANT: DOUGAN,
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US-08-463-875A-1
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                                                                                                                                                                                                                                                                                                                                     Score 175.6; DB 2
Pred. No. 2.6e-39;
0; Mismatches 364
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                  TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                     Query Match 12.6%;
Best Local Similarity 52.6%;
Matches 407; Conservative
                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1980 base pairs
                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                        CDS
395..1822
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                                                                                                                                                                                                                                    , NAME/KEY:
; LOCATION:
US-08-463-875A-1
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996 GAGGTTGTGCAACAACTTATCGAAAAAGGTTTAGTTCAGCGTGGTTGGCTTGGGGTTCAG 1055
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673 agcotgoccaacgaaagotacacaccttcatccaaaccgacgttgccatcaatccgggc 732
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VENTION: METHODS AND COMPOSITIONS FOR METHODS AND ROCHALIMAEA HENSELAE VENTION: AND ROCHALIMAEA QUINTANA INFECTION
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,499
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
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RECISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 1414.612
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 08/245,294
FILING DATE: 18-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08474499; Patent No. 569376; GENERAL INFORMATION: APPLICANT: Anderson, Burt E. APPLICANT: Regnery, Russell L. TITLE OF INVENTION: METHODS AND COTTLLE OF INVENTION: AND ROCHALIMAE NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
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IBM PC compatible
:YSTEM: PC-DOS/MS-DOS
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STATE: Georgia
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APPLICANT: Anderson, Burt E.
APPLICANT: Regnery, Russell L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: INFORMATION: INFORMATION: INFORMATION: INFORMATION: INFORTION
NUMBER OF SEQUENCE: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: 127 Peachtree Street, Suite 1200
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ATTORNEY/AGENT INFORMATION:
NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 1414.612
TELECHONE: 404/688-0770
TELEFAX: 404/688-9880
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APPLICATION NUMBER: US/08/245,29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                   Sequence 7, Application US/08245294
Patent No. 5644047
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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EDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Georgia
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STATE: Georgia
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LOCATION:
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Best Local Si
Matches 403;
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APPLICANT: Regnery, Russell L
TITLE OF INVENTION: Nucleic Acids of Rochalimaea Henselae
TITLE OF INVENTION: and Methods and Compositions for Diagnosing Rochalimaea
TITLE OF INVENTION: Henselae and Rochalimaea Quintana Infection
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                            ADDRESSEE: NEEDLE & ROSENBERG, P.C. STREET: 127 Peachtree Street, N.E., Suite 1200 CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 154.2; DB 1;
Pred. No. 2.1e-33;
0; Mismatches 393;
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/307,279A FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                              Sequence 7, Application US/08307279A Patent No. 5736347
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 1414.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-9880
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1791 base pairs
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Similarity 50.4%;
)3; Conservative C
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                                                                                           GENERAL INFORMATION:
APPLICANT: Anderson,
                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
SOFTWARE: Patentl
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; LOCATION:
US-08-307-279A-7
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Best Local Simi
Matches 403;
                                             US-08-307-279A-7
                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                         STATE:
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Pred. No. 2.1e-33;
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                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                           11.1%;
                                               LENGTH: 1791 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TELEFAX: 404/688-9880
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                             ; NAME/KEY:
; LOCATION:
US-08-474-499-7
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TOPOLOGY: linear
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     nucleic acid
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Best Local Similarity
Matches 403; Conserva
                                STRANDEDNESS:
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; LOCATION:
PCT-US95-06211-7
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US-08-278-091-1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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STREET: 127 Peachtree Street, Suite 1200
CITY: Atlanta
STATE: Georaia
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REFERENCE/DOCKET NUMBER: 1414.6121
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404/688-9880
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 7, Application PC/TUS95062111 ; GENERAL INFORMATION:
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NAME: Spratt, Gwendolyn D.
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CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & RO
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APPLICATION NUMBER: U
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1056 ATTCAGCCTGTAACAAAAATTTCTGATTGAATTGAAGGAGGCTAAAAGGTGCG 1115
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                                                                       Gaps
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      Length 1791;
                                                                    Indels
Score 154.2; DB 4;
Pred. No. 2.1e-33;
0; Mismatches 393;
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1708 GTAAGTGAAGTTTTACCGAAATCTGCTGCAAAAAGCAGGACTTAAAAGCGGGCGATATT 1767
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                                                                                                    856 gregecgaacagetgaaaaacaceggeaaagteeaaegeggaeaaetgggegtgattatt 915
                                                       796 agccgcagcggcggattcatgggcatctcctttgccatcccgattgacgttgccatgaat 855
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APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: COMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1096 gccattacgccgggaaaagaagtcagcctcggcgtatggcgcaaaggcgaa 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1038-495 MIS:vg
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APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/483,859
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
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Patent No. 5656436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 105
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
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COUNTRY: Canada
ZIP: M5G 1R7
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Sequence 1, Application US/08278091
Patent No. 5506139
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with
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APPLICATION NUMBER: US/08/278,091
FILING DATE: 21-JUL-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 139.4; DB 1;
Pred. No. 3.1e-29;
0; Mismatches 381;
                                                                                                                                                                                                                                                                                         ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CTTY: Toronto
STATE: Ontario
COUNTRY: Canada
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 107
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 49.8%;
Matches 384; Conservative
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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US-08-278-091-1
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                       ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                      NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                             OPERATING SYSTEM:
          TITLE OF INVENTION:
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Best Local Similarity
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US-08-472-173-1
                                                                                                                           Canada
                                                                                          CITY: Toronto
STATE: Ontario
                                                                                                                                                                                               COMPUTER:
                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                           COUNTRY:
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                                                                                                                                                                            GATGAACTATCAGATATTGCATTAGTACAGCTTGAAAAACCAAGTAATTTAACAGAAATC 1287
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                                                                                                                             Gaps
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                                                                                       Length 2894;
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APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: COMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with
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                                                                                        DB 1;
                                                                                                                        0; Mismatches 381;
                                                                                       10.0%; Score 139.4; DB 149.8%; Pred. No. 3.1e-29;
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Patent No. 5665353
GENERAL INFORMATION:
                                                                                       Query Match 10.0
Best Local Similarity 49.8
Matches 384; Conservative
; STRANDEDNESS: sir
; TOPOLOGY: linear
US-08-483-859-1
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PatentIn Release #1.0, Version #1.25
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0; Mismatches 381;
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APPLICATION NUMBER: US/08/472,173
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US/08/472,173
FRICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-493 MIS:V9
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 1:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
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                                                                     gtcgccgaacagctgaaaaacaccggcaaagtccaacgcggacaactgggcgtgattatt 915
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Patent No. 5869302
GENERAL INFORMATION:
BAPLICANT: LOOSMORE, Sheena M.
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: COOMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Reduced Protease Activity
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                         1096 gccattacgccgggaaaagaagtcagcctcggcgtatggcgcaaaggcgaa 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: Canada
CIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
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REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-508 MIS:vg
TELECOMMUNICATION INFORMATION:
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FILING DATE: 26-AUG-1994
PRIOR APPLICATION DATA:
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FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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(416) 595-1163
R SEQ ID NO: 1:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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US-08-487-167-1
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APPLICANT: CHONG, Pele APPLICANT: OWEN, Raymond P. APPLICANT: XLEIN, Michel H. TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with Reduced Protease A NUMBER OF SEQUENCES: 23 CORRESPONDENCE ADDRESS:
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    Length 2894;
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Score 139.4; DB 2;
Pred. No. 3.1e-29;
0; Mismatches 381;
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APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
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  10.0%;
49.8%;
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  Query Match
Best Local Simi
Matches 384;
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1648 GGCGAACTCAATGCTGATTTAGCCAAAGCCTTTAATGTAAGCGCGCAACAAGGGCGCATTT 1707
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                                                                   916 caggaagtatcctacggtttggcacagtcgttcggtctggataaagccagcggcqcattg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Analog of Haemophilus Hin47 Protein with
Reduced Protease Activity
                                                                                                                                                                                                                                                                                                                                1096 gccattacgccgggaaaagaagtcagcctcggcgtatggcgcaaaggcgaa 1146
                                                                                                                                                                                                                                                                                                                                                                      1828 ACCACTGGTGCAGGCAAAGAGATTAGCTTGACTTACGTGATGGCAAA 1878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/296,149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.0%; Score 139.4; DB 2;
49.8%; Pred. No. 3.1e-29;
tive 0; Mismatches 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :: Floppy disk
IBM PC compatible
:YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08296149 Patent No. 5939297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOOSMORE, Sheena M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LOOSMORE, Sheena P
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: COMEN, Raymond P.
APPLICANT: KLEIN, MICHEL H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION TELEPHONE: (416) 595-1155 TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2894 base pairs
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: AN
TITLE OF INVENTION: Re
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
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                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATE: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
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Pred. No. 3.1e-29,
Suite 701, 330 University Avenue
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CLASSIFICATION 435
PRIOR APPLICATION NUMBER: 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION NUMBER: US 08/278,091
APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/482,816
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2894 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.0%;
49.8%;
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Best Local Similarity 49.8
Matches 384; Conservative
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STRANDEDNESS: single
                                                                                ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                COUNTRY:
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1408 TCTGACAGTGGCACTTATGAAACTATATATATAAACCGAGCAGCAGCAGCAGCAGCAGCGGGTAAT 1467
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Pred. No. 3.1e-29;
0; Mismatches 381;
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APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,091
                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,816
FILING DATE: 07-JUN-1995
                       US/08/801,499
                                                                                                                                                                                                                                                                                                                                                  NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 101
TELECOMMUNICATION INFORMATION:
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TELEFAX: (416) 595-1163
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 49.8%;
Matches 384; Conservative (
                                                                                                                                                                                                                                                                                                FILING DATE: 21-JUL-1994 ATTORNEY/AGENT INFORMATION:
CURRENT APPLICATION DATA:
                       APPLICATION NUMBER:
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                                               1.168 GATAAAATTACCGTGCAATTACAAGATGGGCGTGAATTTAAAGCAAAATTAGTGGGTAAA 1227
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ggcagtatcaaagtcctgctcaacgacaagcgcgaatataccgccaaactcatcggttcg 501
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6th Floor, 330 University Avenue
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIALE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
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APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
PELICANT: COMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
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CITY: Toronto
STATE: Ontario
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                                                                 1036 giccicagocicgacggcggagaaatacgitcticcgggcgaccitcccgicatggicggc 1095
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APPLICANT: CHONG, Pele
APPLICANT: OOMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: ANALOG OF HAEMOPHILUS HIN47 WITH REDUCED
TITLE OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIM & W-7
STREEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2894;
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APPLICATION NUMBER: US/08/615,271
FILING DATE: 20-JUN-1996
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Pred. No. 3.1e-29;
0; Mismatches 381;
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6th Floor, 330 University Avenue
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IBM PC compatible
:YSTEM: PC-DOS/MS-DOS
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Patent No. 5881503
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: YANG, Yan-Ping
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NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFRENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
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TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2894 base pairs
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Best Local Similarity 49.8%;
Matches 384; Conservative
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MEDIUM TYPE: Floppy
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MOLECULE TYPE:
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COUNTRY:
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Search completed: March 22, 2001, 04:05:10 Job time: 4435 sec

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AA110074 mo51b12.r
                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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AA479844
EST.
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BE236269
BE236299
AV614725
AW462478
AA349615
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134 BE026352
8 AA54554
1 AA028600
141 H16043
13 AA913980
5 AA340884
135 BE754831
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6 BE843509
4 BE055938
AW632119
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D F08513
7 BE335671
I H42958
AW013197
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AA1101392
AA1101392
AW742283
AW742283
AW72620129
AW72620134
AW66844
O F07134
AV667426
A R22703
6 T82703
6 T82703
AV667472
AV6674825
AF179474
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9b_gss26:*
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90-98811::**
90-98813::*
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90-98816::**
90-98818::**
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gb_gss5:*
gb_gss6:*
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gb_gss8:*
gb_gss9:*
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Mammalis Euteria; Filmates; Catalinis, Commission, Commission, Comparation, Contact: Wilson, R. Washungton University School of Medicine Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@waston.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 2408 Std Error: 0.00 Seq primer: -28ml3 rev2 Er from Amersham High quality sequence stop: 417.
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                          Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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               Homo sapiens
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/organism="Mus musculus"
/strain="C57BL/6J"
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/db_xef="taxon:10090"
/clone="UI"-BH3-atr=-02-0-UI"
/clone="UI"-BH3-atr=-02-0-UI"
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/lab_host="UI"-BHAP_M_S4"
/lab_host="Lab_Host"
/cortex, amygdala, basal ganglia, pineal gland, striatum, cortex, amygdala, basal ganglia, pineal gland, striatum, hipoccampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated the following serially subtracted libraries were generated in this process: NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1, libraries in the form of single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mEST@mail.nih.gov

The sequence contained an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first oligonucleotide that was used to prime the synthesis of first strand cond therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the Noti Site and the oligo-dr track served to identify it as a clone from the normalized corpus striatum library cDNA Library Preparation. M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements arrangements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases; 1 to 479)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                UI-W-BH3-atr-e-02-0-UI.sl NIH_BMAP_M_S4 Mus musculus cDNA clone UI-W-BH3-atr-e-02-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Chin, H
National Institute of Mental Health
(6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, 1
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
cgctgttcaacttaaaaggacaggtcgtcggcatcaa 782
                                   Genome Res. 6 (9), 791-806 (1996)
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converted to double-stranded circles and electroporated into DH10B bacteria (LifeTechnologies) to generate the NIH_BMAP_M_S4 library. This procedure has been previously described (Bonabldo, Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_LIB-NIH_BMAP_M_S4
TAG_LIB-NIH_BMAP_M_S4
TAG_LIB-COPPUS-Striatum
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                              Score 98.6; DB 91; Length 479;
Pred. No. 2.5e-17;
0; Mismatches 179; Indels 12
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WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, 1
7el: 314 286 180
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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Unpublished (1996)
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AW742283 660 bp mRNA EST 07-SEP-2000 up55a10.yl Soares_mouse_NMIE Mus musculus cDNA clone IMAGE:2779962 5' similar to TR:092743 092743 NOVEL SERINE PROTEASE. ;, mRNA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
1 (bases 1 to 660)
                                                                                                                                                                                                                                                                                                                                                         /note-"Organ: whole embryo; Vector: pCMV-SPORT2; Site_1: Sali; Site_2: Not1; Cloned unidirectionally. Primcr: Obligo dT. 10.5dpc embryos. pCMV-SPORT2 vector."
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:337879
Seq primer: -28M13 rev1 from Amersham
High quality sequence stop: 446.
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/db_xref="taxon:10090"
/clone="lib-"Life Tech mouse embryo 10 5dpc 10665016"
/tissue_type-"embryo"
/dev_stage="10.5dpc embryos"
/lab_host="DH10B"
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SOURCE
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/organism="Mus musculus"
/strain="C3H x 101 [F1 stock)"
/db_xref="taxon:10090"
/clone="IMAGE:2779962"
/clone="Image:277962"
/clone="Image:277962"
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/dev_stage="newborn"
/lab_host="DH10B"
/dev_stage="newborn"
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                        Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Email: Robert_Strausbergenih.gov
This clone is available royalty free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40RP from Gibco
High quality sequence stop: 431.
Location/Qualifiers
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tive 0; Mismatches 186
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     AUTHORS
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/note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia Notie="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia Notie="Organ: mammary grand constant strand constant str
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 456)
Marra M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Marra M., Hillier, T., Eccy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
    AII59029 456 bp mRNA EST 02-OCT-1998 vz83a08.rl Soares_mammary_gland_NDMMG Mus musculus CDNA clone IMAGE:1333046 5' similar to TR:Q92743 Q92743 NOVEL SERINE PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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Location/Qualifiers
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/db_mare="imAGE:133046"
/clone="imAGE:1333046"
/sex="male"
/tissue_type="mammary_gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
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Pax: 314 286 1810
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53.9%; Pred. No. 2e-16;
tive 0; Mismatches 181;
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Contact: Marra M.Mouse EST Project
Contact: Mouse EST Project
Washi-HHM Mouse EST Project
Washington University School of MedicineP
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The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
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A1159029
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"Vector: pCMV SPORT6; Site_1: Xba1; Site_2: Xho1; Library made from pooled tissue from lymph node, ovary, fat, hypothalanus, and pituitary."
                                                                                                                                    675
                                                                                     250 AGCCCCTTTCTCTTCAAAACACAGTCACCACTGGGATCGTCAGCAGCAGCGAGGG 309
                                                                                                                                                                                                   ------ctgcccaacgaaagctacacccttcatccaaaccgacgttgccatc 723
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   ggttcggatgtccaatccgatgtcgcccttctgaaaatcgacgcaacggaagagctaccc
                                                                 gtcgtcaaaatcggcaatcccaaaaatttgaaaccgggcgaatgggtcgctgccatcggc
                                                                                                                                  616 gegecetteggetttgacaacagegtgacegecggeategtgteegecaaaggeagaage
                                130 GATGTGGATGAAAAGGCGGACATTGCGCTTATCAAGATTGACCACCAGGGAAAGCTGCCA
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                                                                                                                                                                                                                                                                                                                                                                         AW654015 521 bp mRNA EST 103226 MARC 1BOV Bos taurus CDNA 5', mRNA sequence. AW654015 GI:7419841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TED: 402 762 4890
Fax: 402 762 4390
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/clone_lib="MARC 1BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plate: 103 row: D column: 5
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
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/lab_host="DH10B"
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Contact: Smith TPL
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 474)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Mucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
Coptact: Wilson RK
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/dev_stage="19 weeks"
/lab_hostu="DH10B (ampicillin resistant)"
/note="Organ: lung; Vector: pT773D (Pharmacia) with a
modified polylinker; Site_l: Not I; Site_2: Eco RI; 1st
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This clone is available royalty-free through LLNL; contact the
TMAGE Consortuum (info@image.linl.gov) for further information.
Seq primer: ETPrimer
High quality sequence stop: 446.
Location/Qualiflers
                                    545
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IMAGE:302294 5' similar to SW:HTRA_SALTY P26982 PROTEASE DO
PRECURSOR ;, mRNA sequence.
                                                                                                          486 caaactcatcggttcggatgtccaatccgatgtcgcccttctgaaaatcgacgcaacgga
                                                                                                                                         546 agagetaccegtegteaaaateggeaateceaaaaatttgaaaeeegggegaatgygtege
                                                                                                                                                                                                                                                                                                                          606 tgccatcggcgcccttcggctttgacaacagcgtgaccgccggcatcgtgtccgccaa
                                                                                                                                                                                                                                                                                                                                                            308 GGCCATTGGAAGCCCGTTTTCCCTTCAAAACACGGGTCACCACGGGGATCGTCAGCACCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                        666 aggcag-----aagcctgcccaacgaaagctacacaccttcatccauaccga
426 cgtcgttgccggtatgggcagtatcaaagtcctgctcaacgacaagcgcgaatalaccgc
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/db_xref="GDB:1247226"
/db_xref="taxon:9606"
/clone="IMAGE:302294"
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W17262.1 GI:1291697
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illarity 57.4%;
Conservative
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Matches 166; Conserv
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1 (bases I to 485)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Walliamson,A., Wohldmann,P. and Wilson,R.

The WashU-marck EST Project
Contact: Wilson RK
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double-stranded cDNA was size selected, ligated to Eco Ri adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco Ri sites of a modified pT773 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart 185 g 93 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
Insert Size: 1476
High quality sequence stops: 391 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1476 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                           41 GGGTCTGGGTTTATTGTGTCGGAAGATGGACTGATCGTGACAAATGCCCACGTGGTGACC 100
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yg75a09.rl Soares infant brain 1NIB Homo sapiens CDNA clone
IMAGE:38967 5' similar to SP:HTRA_SALTY P26982 PROTEASE DO
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                       Score 92.2; DB 146; Length 474; Pred. No. 1.6e-15;
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Best Local Similarity 57.4%;
Matches 166; Conservative
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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DO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
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/organism="Homo sapiens"
/db_xref="GB141508"
/db_xref="taxon:9606"
/clone="IMAGE:38967"
/clone=llb=Soares infant brain INIB"
/sex="female"
/dev_stage="77"
/de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 92.2; DB 144;
Pred. No. 1.6e-15;
0; Mismatches 123;
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Email: genexpress@genethon.fr
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v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
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Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B., Lorenzo, F., Mitchell, Mariage-Samson, R., Pietu, G., Pouliot, Y., Sebastiani-Kabaktchis, and Tessier, A.

IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                                                                                                                                               /note-"vector: pcMv SPORT6; Site_1: Xba1; Site_2: Xho1; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 caaactcatcggttcggatgtccaatccgatgtcgcccttctgaaaatcgacgaacgga 545
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HSC1WG081 normalized infant brain cDNA Homo sapiens cDNA clone
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Genethon Centre de recherche sur le Genome Humain
1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
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                                                                                                                                                                                                                                                                                                                                                                                                   Length 504;
                                                                                                                                                                                                                                                                                                                                                                                               6.5%; Score 91; DB 93; Length 50 llarity 56.5%; Pred. No. 3.6e-15; Conservative 0; Mismatches 130; Indels
                                                                                                                                                                                                        /clone_lib="MARC 1BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                     1. 504
/organism~"Bos taurus"
/db_xref="taxon:9913"
                                                                        BACKWARD: GTTTTCCCAGTCACGACG
Plate: 101 row: N column: 22
Seg primer: ATTTAGGTGACACTATAG.
                                     PCR PRIMERS
FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                   Location/Qualifiers
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/Basue_type="total brain"
/dev_stage="3 months old"
/dev_stage="3 months old"
/dev_stage="3 months old"
/dete="forgan: brain; Vector: lafmid BA; Site=1: HindIII;
Site=2: NotI; sex=Female; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total brain;
total mRNA was oligo=(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychlatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"
a 95 c 100 g 66 t lothers
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1 (bases 1 to 529)
Sugimoto,Y., Hirotsune,S., Takasuga,A., Itoh,R., Jitchzono,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              376 ggttcgggcttcatcatcagcaaaaacggctacatcctgaccaatacccacgtcgttgcc 435
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Bovine CDNA sequencing

Dovine CDNA sequencing

Unpublished (2000)

Contact: Yoshikazu Sugimoto

Animal Genetics Division

Shirakava Institute of Animal Genetics

Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan

Tel: 81-248-25-5641
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/db_xref="taxon:9606"
/clone="c-lwg08"
/clone=lib="normalized infant brain cDNA"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 89.6; DB 140; Length
Pred. No. 8.2e-15;
0; Mismatches 125; Indels
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AV614726.1 GI:9750396
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Best Local Similarity 56.7%;
Matches 164; Conservative
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Tel: +55-11-2704922
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1 (bases 1 to 559)
                                                                                           /organism="Bos taurus"
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/clone="ElAD006406"
/clone_lib="Bos taurus adipocyte cell line"
/cell_type="an adipocyte cell line"
/lab_host="DH108"
/note="Vector: pZL1; Site_1: Sal1; Site_2: Not1; Poly A was deleted from a Not1 site"
a 139 c 149 g 108 t l others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                290 AAAGCIGCCIGIGCIACTGCTIGGCCGCTCCICGGAGCIGCGGCGGGGAGAGIICGIGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          caaactcatcggttcggatgtccaatccgatgtcgcccttctgaaaatcgacgcaacgga
Fax: 81-248-25-5725
Email: kazusugi@cocoa.ocn.ne.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
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W599976 Bos taurus cartilage fetus Bos taurus cDNA clone
E1CA047C06 5′, mRNA sequence.
AV599976
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                                                                                                                                                                                                                                                                                      Length 529;
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Pred. No. 1.4e-14;
0; Mismatches 185; Indels
                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 337)
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158 c 158 g 108 t
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
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QV-BT032-190299-136 BT032 Homo sapiens cDNA, mRNA sequence.
A1903651
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                                                                              Single pass sequencing. This clone was obtained from a polyA-deleted cDNA library.
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/ Organism="Bos taurus"
/db_xref="taxon:9913"
/clone_rE1CA047c06"
/clone_lib="Bos taurus cartilage fetus"
/tissue_type="cartilage"
/dev_stage="fetus"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 87.8; DB 37;
Pred. No. 3.1e-14;
0; Mismatches 132;
Tel: 81-248-25-5641
Fax: 81-248-25-5725
Email: kazusugi@cocoa.ocn.ne.jp
                                                                                                                                      Location/Qualifiers
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Matches 167; Conservative
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Unpublished (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A minil-library was made by clothing products derived from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the puc 18 Vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
Fax: +55-11-2707001
Email: asImpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?tl=QV&t2=QV-BT032-136.html
&t3=190299&t4=1)
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55:9%; Pred. No. 7.6e-14;
tive 0; Mismatches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 t
                                                                                                                                                                                                                                                                                                   /organism-"Homo sapiens"
/db_xref-"taxon:9606"
/clone_lib="BT032"
/sex-"female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cgtgaccgccggcatcgtgtccgccaaaggc 669
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                                                                                                                                                                                                      Seq primer: puc 18 forward.
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Matches 185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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SOURCE
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Contact: Wilson RW
Washington University School of Medicine
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estéwatson.wustl.edu
Insert Size: 1522
High quality sequence stops: 453 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       436 ggtatgggcagtatcaaagtcctgctcaacgacaagcgcgaatataccgccaaactcatc 495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 Greergerregecegreercagagergegecegecegeantregreerecearceca 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [9
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Pred. No. 3.2e-13;
); Mismatches 120; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone-"IMAGE:31324"
/clone_lib-"Soares infant brain 1NIB"
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/db_xref="GDB:403671"
/db_xref="taxon:9606"
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High quality sequence stop: 453
Location/qualiflers
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Best Local Similarity
Matches 155; Conserv
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Job time: 4478 sec

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 288) House, To 288; To 288; To 288; To 288; M., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lafmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                  Email: estewatson.wustl.edu
Insert Size: 1530
High quality sequence stops: 143 Source: IMAGE Consortium, LLNL
This clone is available royalty free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Insert Length: 1530 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                374 teggitegggetteateateageaaaaeggetacateetgaeeaataeeeagtegitg 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 CCAACAAGCACCGGGTCAAAGTTGAGCTGAAGAACGGTGCCACTTACGAAGCCAAAATCA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   494 toggttoggatgtccaatccgatgtcgcccttctgaaaatcgacgcaacggaagagctac 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             554 ccgtcgtcaaaatcggcaatcccaaaaatttgaaaccgggcgaatgggtcgctgccatcg 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 CTGTCCTGCTNCTTTGCCNCTCCTCAGAGCTGCGGNCNGGAGAGTTCGTNGTCNCCATCG 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                             Contact: Wilson Rk
Washington University School of Medicine
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 146; Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.8%; Score 81.2; DB 146; Length
53.7%; Pred. No. 1.9e-12;
tive 0; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
/clone="IMAGE:24795"
/clone_lib="Soares infant brain INIB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gegeeectteggetttgacaacagegtgaccgeeggeategt 656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="GDB:397142"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 143.
Location/Qualifiers
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